

REMARKS/ARGUMENTS

Claims 20-28, 30, and 46-48 are active. Claim 46 was indicated as allowable. Claims 29 and 31-45 have been withdrawn from consideration. Claim 47 has been separated into claims 47 and 48 as suggested by the Examiner. The claims have been amended to refer to polypeptides which are about 35kD. Support for this limitation is found in the specification on page 1, line 4 and on page 4, 5th line from the bottom. No new matter has been added. Favorable consideration of this Amendment and allowance of this application is now respectfully requested.

Restriction/Election

The Applicants previously elected with traverse Group I, Claims 1, 2, 4, 5, 7 and 18 and made a second election of SEQ ID NO: 1 (a human sequence, SEQ ID NO: 3 is the corresponding rat sequence). SEQ ID NOS: 1 and 3 encode the amino acid sequences of SEQ ID NOS: 2 and 4. According to page 39, line 4, of the specification, the amino acid sequences of SEQ ID NOS: 2 (human) and 4 (rat) have 87% homology. Moreover, the human and rat polynucleotide sequences each fall within the first election of Group I. In view of the relatedness of these sequences, the Applicants request that the restriction requirement between the human and rat sequences be withdrawn.

The Applicants thank the Examiner for indicating that Claims 29 will be rejoined. Claim 44 was withdrawn, but depends solely from elected Claim 30, therefore this claim should be rejoined.

It is also respectfully requested that the claims of the nonelected group(s) which depend from or otherwise include all the limitations of an allowed elected claim, be rejoined upon an indication of allowability for the elected claim, see MPEP 821.04.

Rejection—35 U.S.C. 102

Claims 20-28, 30 and 47 were rejected under 35 U.S.C. 102(a) and (e) as being anticipated by Tang et al., U.S. 60/336,453, and Strausberg et al., PNAS 99:16899. These rejections are moot in view of the amendments above which require that the polynucleotide encode a polypeptide of about 35kD. While positions 419-1399 of the Tang sequence were shown to align to SEQ ID NO: 1, Tang does not disclose a polynucleotide sequence consisting of a coding region for a polypeptide having a molecular weight of about 35 kD. Similarly, Strausberg's sequence is much longer than the polynucleotide of Claim 20. Moreover, neither Tang nor Strausberg provides any motivation for selecting a fragment of their longer sequences that encodes a polypeptide having a molecular weight of about 35kD which binds to WF00144. The Applicants also reiterate their earlier arguments that these documents do not disclose the invention with sufficient specificity to anticipate it. Accordingly, the Applicants respectfully request that this rejection be withdrawn.

Rejection—35 U.S.C. 102

Claim 21 and 30 were rejected under 35 U.S.C. 102(a) and (e) as being anticipated by Valenzuela et al., WO 2000/49134. This rejection is moot in view of the amendments above which require a polynucleotide that encodes a polypeptide that binds to WF00144 which has a molecular weight of about 35 kD. Valenzuela discloses a short sequence alignment between nucleotides 752-770 of SEQ ID NO: 1 and a sequence in the search database. However, it does not disclose the longer 96% homologous polynucleotide sequence required by the claims, nor provide any suggestion of such a sequence. Accordingly, the Applicants respectfully request that this rejection be withdrawn.

Issues raised by Advisory Action

To speed prosecution, the Applicants respond below to the new issues set forth in the Advisory Action. (The prior art rejections are discussed above.)

1. The Applicants thank the Examiner for indicating that the non-elected composition of claim 44 will be rejoined upon allowance of product claim 30.

2. Claim 20 has been revised to emphasize that the polynucleotide has homology to

SEQ ID NO: 1.

3. Claim 20 provides proper antecedent basis for the term "at least 95% homology" or for the hybridization conditions in claim 22, because these limitations further limit the scope of claim 20. For example, claim 20 encompasses both cross-hybridizing sequences and sequences having at least 96% homology, while claims 21 and 22 are specifically directed to one or the other.

4. Claim 47 has been revised as suggested.

5. The Applicants thank the Examiner for indicating that the amendment of claim 30 would overcome a rejection.

CONCLUSION

In view of the above amendments and remarks, the Applicants respectfully submit that this application is now in condition for allowance. Early notification of such is earnestly requested.

Respectfully submitted,

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